Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-35. (canceled)

36. (currently amended) A method of identifying mutations in a sample nucleic acid sequence, said method comprising ~~the steps of~~:

storing plurality of patterns in a library, each pattern corresponding to a region including multiple base positions where probe intensities reflecting hyridization affinity to a first nucleic acid sequence differ from probe intensities reflecting hybridization affinity to a second nucleic acid sequence and wherein the first and second nucleic acid sequences differ at a base position within the region;

comparing a pattern to the patterns in the ~~libraray~~ library, the pattern corresponding to a region including multiple base positions where probe intensities reflecting hybridization affinity to a reference nucleic acid sequence differ from probe intensities reflecting hybridization affinity to a sample nucleic acid sequence; and

identifying a mutation in the sample nucleic acid sequence according to at least a ~~match~~ ratio and ~~with~~ a pattern in the library.

37. (previously presented) The method of claim 36, wherein a shape of the patterns in the library vary according to the destabilization associated with the different bases at the base position within the region.

38. (previously presented) The method of claim 36, wherein the probe intensities reflect hybridization affinity of wild-type probes.

39. (currently amended) The method of claim 36, wherein:

probes corresponding to the probe intensities have a length and an interrogation position;

the base position of the mutation in the sample nucleic acid sequence is identified utilizing the length of the probes and the interrogation position.

40. (canceled)

41. (currently amended) A computer program product stored in a computer readable medium for identifying mutations in a sample nucleic acid sequence, comprising:

computer readable code that store a plurality of patterns in a ~~libraray~~ library, each pattern corresponding to a region including multiple base positions where probe intensities reflecting hybridization affinity to a first nucleic acid sequence differ from probe intensities reflecting hybridization affinity to a second nucleic acid sequence and wherein the first and second nucleic acid sequences differ at a base position within the region;

computer code that compares a pattern to the patterns in the library, the pattern corresponding to a region including multiple base positions where probe intensities reflecting hybridization affinity to a reference nucleic acid sequence differ from probe intensities reflecting hybridization affinity to a sample nucleic acid sequence;

computer code that identifies a mutation in the sample nucleic acid sequence according to at least a ~~match~~ ratio and ~~with~~ a pattern in the library; and

a tangible medium that stores said computer readable codes.

42. (previously presented) The computer program product of claim 41, wherein a shape of the patterns in the library vary according to the destabilization associated with the different bases at the base position within the region.

43. (previously presented) The computer program product of claim 41, wherein the probe intensities reflect hybridization affinity of wild-type probes.

44. (currently amended) The computer program product of claim 41, wherein:

the probes corresponding to the probe intensities have a length and an interrogation position;

the base position of the mutation in the sample nucleic acid sequence is identified utilizing the length of the probes and the interrogation position.

45. (canceled)